

SCORE Search Results Details for Application 09586625 and Search Result us-09-586-625-1.rng.

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 12:11:09 ; Search time 3788 Seconds
(without alignments)
12567.717 Million cell updates/sec

Title: US-09-586-625-1
Perfect score: 6828
Sequence: 1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 13:23:40 ; Search time 28834 Seconds
(without alignments)
13241.909 Million cell updates/sec

Title: US-09-586-625-1
Perfect score: 6828
Sequence: 1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

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OM nucleic - nucleic search, using sw model

```
Run on:      July 26, 2006, 13:38:41 ; Search time 795 Seconds
              (without alignments)
              16070.353 Million cell updates/sec
```

```
Title:          US-09-586-625-1
Perfect score:  6828
Sequence:       1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_NA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2006, 23:01:51 ; Search time 637 Seconds
(without alignments)
16384.827 Million cell updates/sec

Title: US-09-586-625-1
Perfect score: 6828
Sequence: 1 gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

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SUMMARIES

Result No.	Score	% Match	Query Length	IDB	Description

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OM nucleic - nucleic search, using sw model

```
Run on:      July 26, 2006, 13:38:41 ; Search time 795 Seconds
              (without alignments)
              16070.353 Million cell updates/sec
```

```
Title:          US-09-586-625-1
Perfect score:  6828
Sequence:       1  gacggatcgggagatctccc.....gaaaagtgccacctgacgtc 6828
```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_NA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES